IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: **US/10/811,138**

DATE: 09/14/2004
TIME: 10:27:35

Input Set : **A:\US Utility 050229-0421 Sequence Listing.txt**
Output Set: **N:\CRF4\09142004\J811138.raw**

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 3 <110> APPLICANT: University of Kentucky Research Foundation
 4        Daunert, Sylvia
 5        Rowe, Laura
 6        Dikici, Emre
 7        Deo, Sapna Kamalakar
 9 <120> TITLE OF INVENTION: AEQUORIN AND OBELIN MUTANTS WITH DIFFERING WAVELENGTHS AND
10        BIOLUMINESCENCE
12 <130> FILE REFERENCE: 050229-0421
14 <140> CURRENT APPLICATION NUMBER: 10/811,138
15 <141> CURRENT FILING DATE: 2004-03-29
17 <160> NUMBER OF SEQ ID NOS: 6
19 <170> SOFTWARE: PatentIn version 3.2
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 861
23 <212> TYPE: DNA
24 <213> ORGANISM: Aequorea victoria
26 <400> SEQUENCE: 1
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29 tctcgacaac aacaagcaaa catgacaagc aaacaatact cagtcaagct tacatcagac   120
31 ttcgacaacc caagatggat tggacgacac aagcatatgt tcaatttcct tgatgtcaac   180
33 cacaatggaa aaatctctct tgacgagatg gtctacaagg catctgatat tgtcatcaat   240
35 aaccttggag caacacctga gcaagccaaa cgacacaaag atgctgtaga agccttcttc   300
37 ggaggagctg gaatgaaata tggtgtggaa actgattggc ctgcatatat tgaaggatgg   360
39 aaaaaattgg ctactgatga attggagaaa tacgccaaaa acgaaccaac gctcatccgt   420
41 atatggggtg atgctttgtt tgatatcgtt gacaaagatc aaaatggagc cattacactg   480
43 gatgaatgga agcatacac  caaagctgct ggtatcatcc aatcatcaga agattgcgag   540
45 gaaacattca gagtgtgcga tattgatgaa agtggacaac tcgatgttga tgagatgaca   600
47 agacaacatt taggattttg gtacaccatg gatcctgctt gcgaaaagct ctacggtgga   660
49 gctgtcccct aagaagctct acggtggtga tgcaccctgg gaagatgatg tgattttgaa   720
51 taaaacactg atgaattcaa tcaaaatttt ccaaattttt gaacgatttc aatcgtttgt   780
53 gttgattttt gtaattagga acagattaaa tcgaatgatt agttgttttt ttaatcaaca   840
55 gaacttacaa atcgaaaaag t                                             861
58 <210> SEQ ID NO: 2
59 <211> LENGTH: 189
60 <212> TYPE: PRT
61 <213> ORGANISM: Aequorea victoria
63 <400> SEQUENCE: 2
65 Val Lys Leu Thr Ser Asp Phe Asp Asn Pro Arg Trp Ile Gly Arg His
66 1               5                   10                  15
69 Lys His Met Phe Asn Phe Leu Asp Val Asn His Asn Gly Lys Ile Ser
70              20                  25                  30
73 Leu Asp Glu Met Val Tyr Lys Ala Ser Asp Ile Val Ile Asn Asn Leu
74          35                  40                  45
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77  Gly Ala Thr Pro Glu Gln Ala Lys Arg His Lys Asp Ala Val Glu Ala
78      50                  55                  60
81  Phe Phe Gly Gly Ala Gly Met Lys Tyr Gly Val Glu Thr Asp Trp Pro
82 65                  70                  75                  80
85  Ala Tyr Ile Glu Gly Trp Lys Lys Leu Ala Thr Asp Glu Leu Glu Lys
86                      85                  90                  95
89  Tyr Ala Lys Asn Glu Pro Thr Leu Ile Arg Ile Trp Gly Asp Ala Leu
90                  100                 105                 110
93  Phe Asp Ile Val Asp Lys Asp Gln Asn Gly Ala Ile Thr Leu Asp Glu
94              115                 120                 125
97  Trp Lys Ala Tyr Thr Lys Ala Ala Gly Ile Ile Gln Ser Ser Glu Asp
98          130                 135                 140
101 Cys Glu Glu Thr Phe Arg Val Cys Asp Ile Asp Glu Ser Gly Gln Leu
102 145                 150                 155                 160
105 Asp Val Asp Glu Met Thr Arg Gln His Leu Gly Phe Trp Tyr Thr Met
106                 165                 170                 175
109 Asp Pro Ala Cys Glu Lys Leu Tyr Gly Gly Ala Val Pro
110             180                 185
113 <210> SEQ ID NO: 3
114 <211> LENGTH: 861
115 <212> TYPE: DNA
116 <213> ORGANISM: Aequorea victoria
118 <400> SEQUENCE: 3
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123 ttcgacaacc caagatggat tggacgacac aagcatatgt tcaatttcct tgatgtcaac     180
125 cacaatggaa aaatctctct tgacgagatg gtctacaagg catctgatat tgtcatcaat     240
127 aaccttggag caacacctga gcaagccaaa cgacacaaag atgctgtaga agccttcttc     300
129 ggaggagctg gaatgaaata tggtgtggaa actgattggc ctgcatatat tgaaggatgg     360
131 aaaaaattgg ctactgatga attggagaaa tacgccaaaa acgaaccaac gctcatccgt     420
133 atatggggtg atgctttgtt tgatatcgtt gacaaagatc aaaatggagc cattacactg     480
135 gatgaatgga agcatacac caaagctgct ggtatcatcc aatcatcaga agatagcgag     540
137 gaaacattca gagtgagcga tattgatgaa agtggacaac tcgatgttga tgagatgaca     600
139 agacaacatt taggattttg gtacaccatg gatcctgcta gcgaaaagct ctacggtgga     660
141 gctgtcccct aagaagctct acggtggtga tgcaccctgg aagatgatg tgattttgaa     720
143 taaaacactg atgaattcaa tcaaaatttt ccaaattttt gaacgatttc aatcgtttgt     780
145 gttgattttt gtaattagga acagattaaa tcgaatgatt agttgttttt ttaatcaaca     840
147 gaacttacaa atcgaaaaag t                                               861
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151 <211> LENGTH: 189
152 <212> TYPE: PRT
153 <213> ORGANISM: Aequorea victoria
155 <400> SEQUENCE: 4
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158 1               5                   10                  15
161 Lys His Met Phe Asn Phe Leu Asp Val Asn His Asn Gly Lys Ile Ser
162              20                  25                  30
165 Leu Asp Glu Met Val Tyr Lys Ala Ser Asp Ile Val Ile Asn Asn Leu
166          35                  40                  45
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169 Gly Ala Thr Pro Glu Gln Ala Lys Arg His Lys Asp Ala Val Glu Ala
170     50                  55                  60
173 Phe Phe Gly Gly Ala Gly Met Lys Tyr Gly Val Glu Thr Asp Trp Pro
174 65                  70                  75                  80
177 Ala Tyr Ile Glu Gly Trp Lys Lys Leu Ala Thr Asp Glu Leu Glu Lys
178             85                  90                  95
181 Tyr Ala Lys Asn Glu Pro Thr Leu Ile Arg Ile Trp Gly Asp Ala Leu
182         100                 105                 110
185 Phe Asp Ile Val Asp Lys Asp Gln Asn Gly Ala Ile Thr Leu Asp Glu
186         115                 120                 125
189 Trp Lys Ala Tyr Thr Lys Ala Ala Gly Ile Ile Gln Ser Ser Glu Asp
190     130                 135                 140
193 Ser Glu Glu Thr Phe Arg Val Ser Asp Ile Asp Glu Ser Gly Gln Leu
194 145                 150                 155                 160
197 Asp Val Asp Glu Met Thr Arg Gln His Leu Gly Phe Trp Tyr Thr Met
198             165                 170                 175
201 Asp Pro Ala Ser Glu Lys Leu Tyr Gly Gly Ala Val Pro
202             180                 185
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206 <211> LENGTH: 662
207 <212> TYPE: DNA
208 <213> ORGANISM: Obelia longissima
210 <400> SEQUENCE: 5
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213 aatgtcttca aaatacgcag ttaaactcaa gactgacttt gataatccac gatggatcaa   120
215 aagacacaag cacatgtttg atttcctcga catcaatgga aatggaaaaa tcaccctcga   180
217 tgaaattgtg tccaaggcat ctgatgacat atgtgccaag ctcgaagcca caccagaaca   240
219 aacaaaacgc catcaagttt gtgttgaagc tttctttaga ggatgtggaa tggaatatgg   300
221 taaagaaatt gccttcccac aattcctcga tggatggaaa caattggcga cttcagaact   360
223 caagaaatgg gcaagaaacg aacctactct cattcgtgaa tggggagatg ctgtctttga   420
225 tattttcgac aaagatggaa gtggtacaat cactttggac gaatggaaag cttatggaaa   480
227 aatctctggt atctctccat cacaagaaga ttgtgaagcg acatttcgac attgcgattt   540
229 ggacaacagt ggtgaccttg atgttgacga gatgacaaga caacatcttg gattctggta   600
231 cactttggac ccagaagctg atggtctcta tggcaacgga gttccctaag cttttttttcg   660
233 aa                                                                   662
236 <210> SEQ ID NO: 6
237 <211> LENGTH: 195
238 <212> TYPE: PRT
239 <213> ORGANISM: Obelia longissima
241 <400> SEQUENCE: 6
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247 Arg Trp Ile Lys Arg His Lys His Met Phe Asp Phe Leu Asp Ile Asn
248             20                  25                  30
251 Gly Asn Gly Lys Ile Thr Leu Asp Glu Ile Val Ser Lys Ala Ser Asp
252             35                  40                  45
255 Asp Ile Cys Ala Lys Leu Glu Ala Thr Pro Glu Gln Thr Lys Arg His
256     50                  55                  60
259 Gln Val Cys Val Glu Ala Phe Phe Arg Gly Cys Gly Met Glu Tyr Gly
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260 65                      70              75                  80
263 Lys Glu Ile Ala Phe Pro Gln Phe Leu Asp Gly Trp Lys Gln Leu Ala
264                 85              90              95
267 Thr Ser Glu Leu Lys Lys Trp Ala Arg Asn Glu Pro Thr Leu Ile Arg
268                 100             105             110
271 Glu Trp Gly Asp Ala Val Phe Asp Ile Phe Asp Lys Asp Gly Ser Gly
272         115             120             125
275 Thr Ile Thr Leu Asp Glu Trp Lys Ala Tyr Gly Lys Ile Ser Gly Ile
276     130             135             140
279 Ser Pro Ser Gln Glu Asp Cys Glu Ala Thr Phe Arg His Cys Asp Leu
280 145             150             155             160
283 Asp Asn Ser Gly Asp Leu Asp Val Asp Glu Met Thr Arg Gln His Leu
284             165             170             175
287 Gly Phe Trp Tyr Thr Leu Asp Pro Glu Ala Asp Gly Leu Tyr Gly Asn
288         180             185             190
291 Gly Val Pro
292         195
```

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